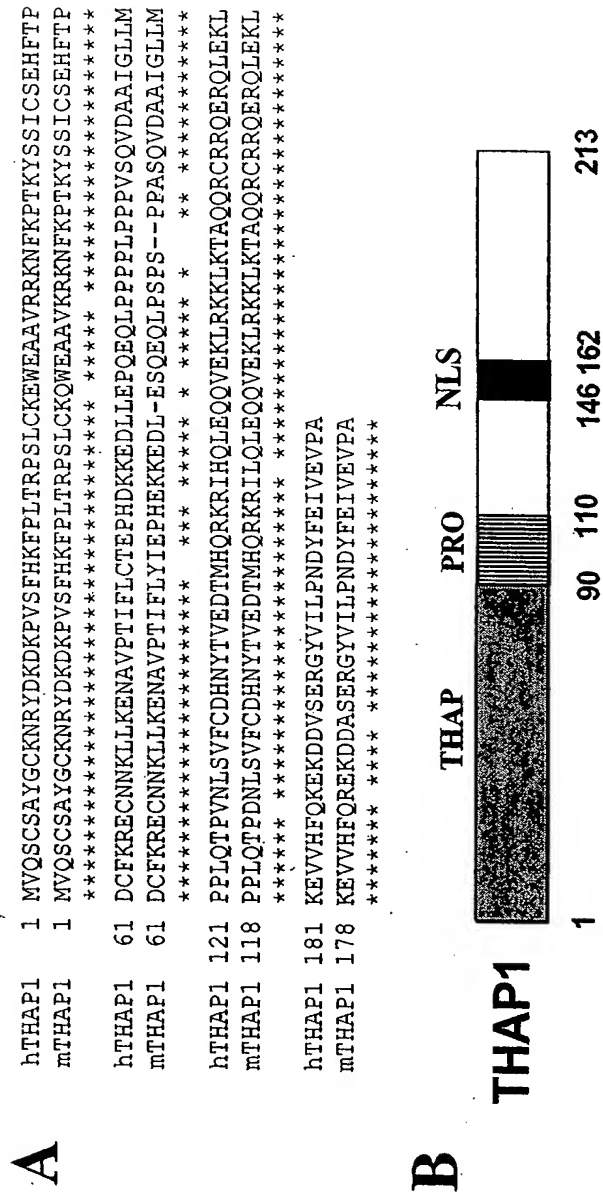


FIGURE 1



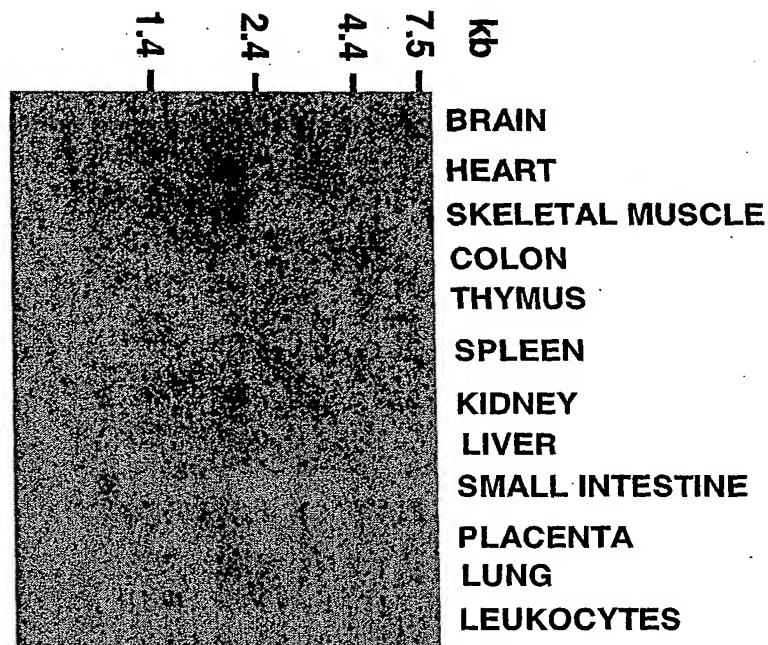


FIGURE 2

Figure 3

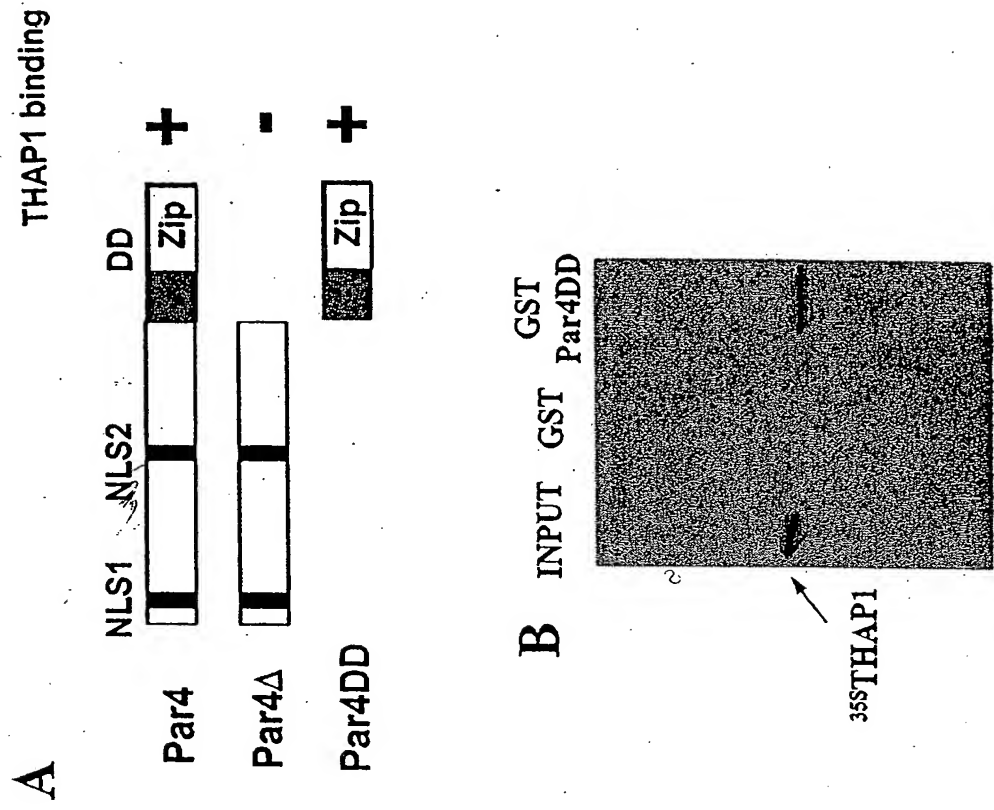


FIGURE 4A

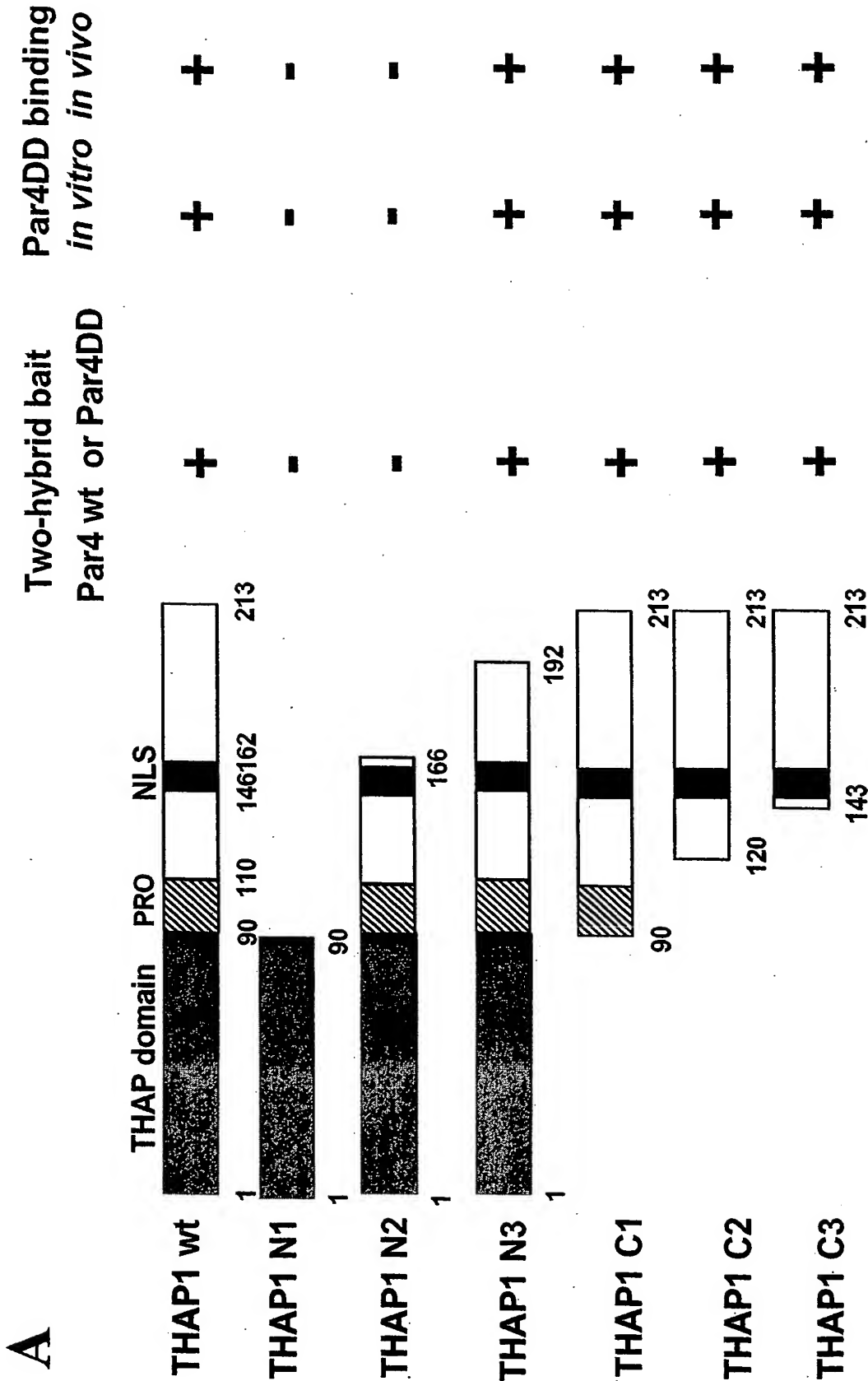


Figure 4b

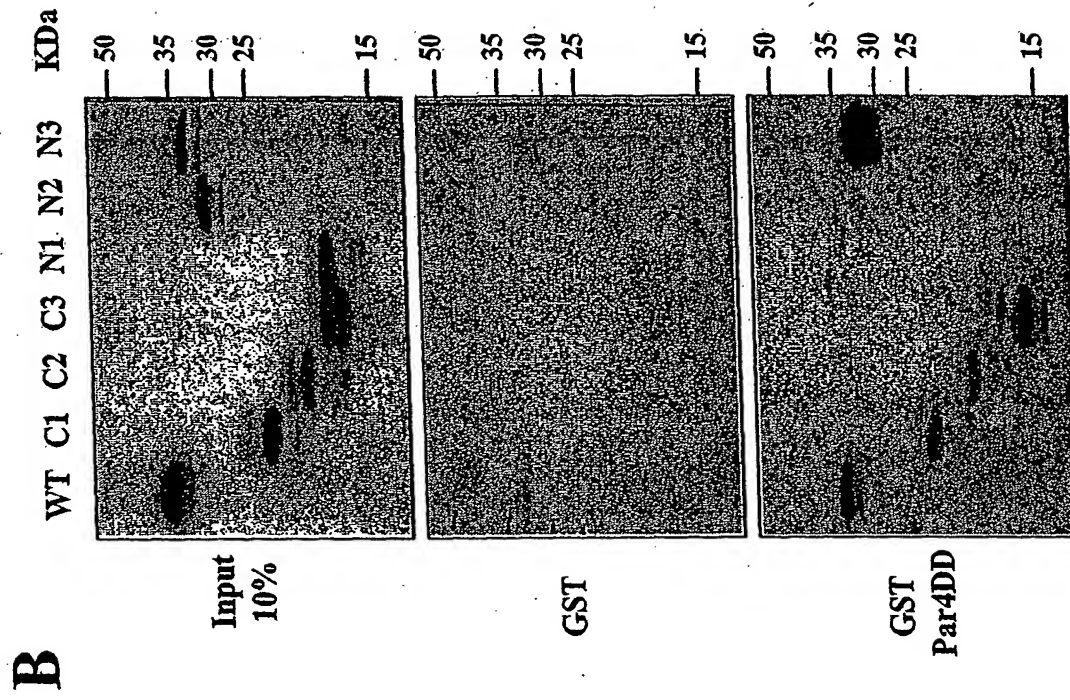


Figure 5

A

mZIP -VLEDVAAAEQGLREL--QRGRRCRERVCAALRAAAEQ**E**ARCRDG
 mTHAP-1 -QLEQQVEKLRRKKLKTAAQ**QRCRRQ**ERQLEKLKEVVF**QRE**KDDASE
 hTHAP-1 -QLEQQVEKLRRKKLKTAAQ**QRCRRQ**ERQLEKLKEVVF**QRE**KDDDVSE

Consensus Par4 binding site: LE (X₁₂₋₁₄) QRXRRQXR (X₁₁) QXE

B

Two-hybrid bait Par4DD binding
 Par4 wt or Par4DD *in vitro* *in vivo*

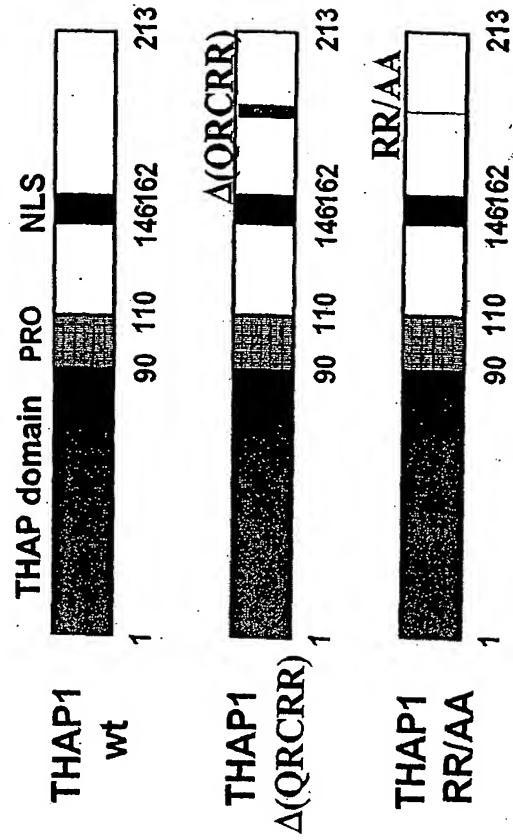


Figure 6

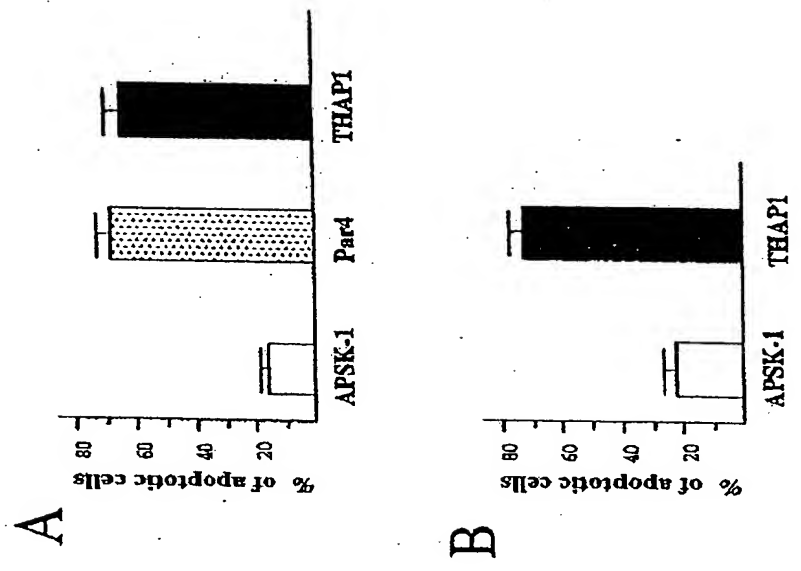


Figure 7

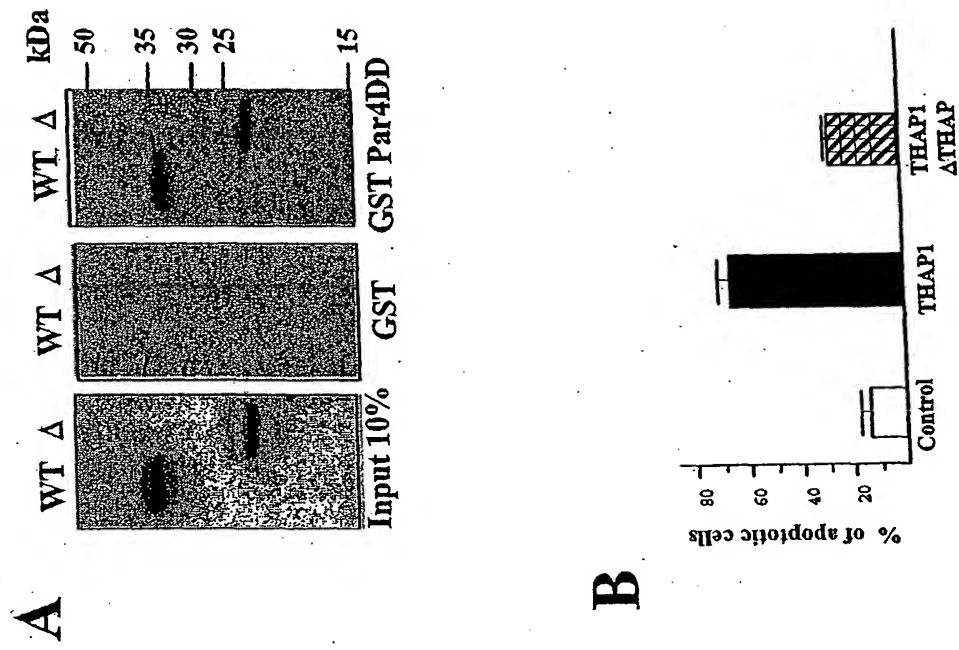


Figure 8

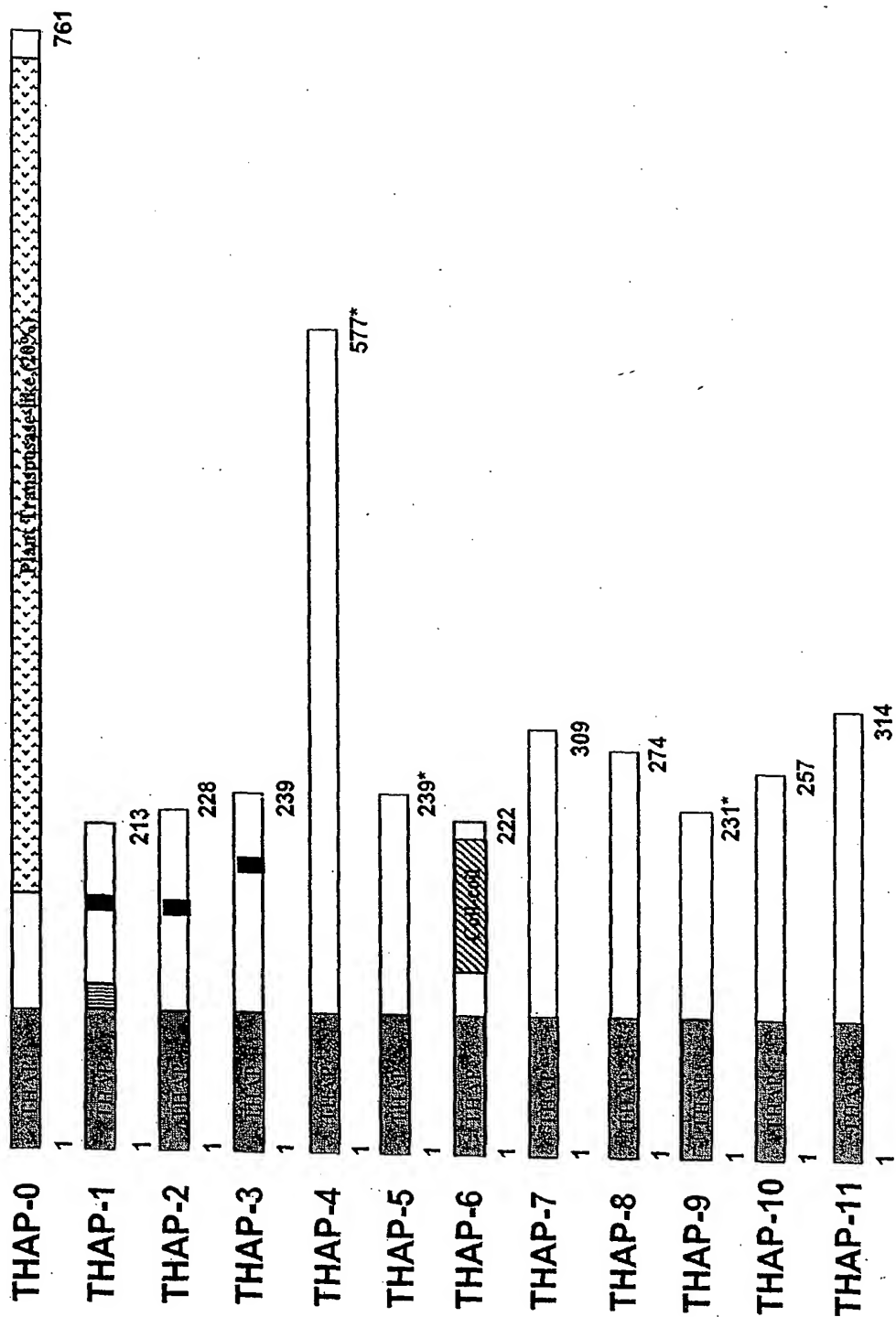


Figure 9

A

hTHAP1 1 MVOSCSAAGCKNRDYDKMPVSEHFPPITRPSLOKMEAAVRRKNEKPKTKYSSIGSEHETP
 dmTransposase 1 -MKYC-RECK-AVTGVTHHVPICALRR---KMEOSLG---CSLGENSEQICDTHEND
 consensus 1 mv Cs y CKn K v K l Rpslck WE v rkn S lC HF

hTHAP1 61 DQEK-----RECNNKIKENAVPTIFICTEPHDK
 dmTransposase 51 SQKKAAPAKGQTEKRPINADAVEKVIHPEPEKI
 consensus 61 fKaapakg k l AVpt l EP

B

hTHAP1 1 MVOSCSAAGCKNRDYDKMPVSEHFPPITRPSLOKMEAAVRRKNEKPKTKYSSIGSEHETP
 hTHAP3 1 MEYS-SARCS-CHYSS---KQHTVIGSEHFPECE-SAPGN---NRIKKNNAVPTIFICTEPHDK
 hTHAP5 1 MEKX-SANIC-CKMRGRNKKD-RKISFYFTHIDTKLEKIANKK-RDS---RKNKKNNAVPTIFAFQDFTQ
 hTHAP8 1 MEKX-SANIC-SHAGRLGADNRPSSEKPELKHGLOQAMHORG-CEH---VRLKPECAVPSIFSGPPAK
 hTHAP4 1 VVIC-SAVNCS-SURQCK-GENRQSTHIFPILDSRLICQKRWQ-SDN---CHRLKPECAVPSIFH--LTK-
 hTHAP2 1 MTN-SANACATYN---RHINSHIFPILDPHCKEMRLR-RKN---TR-RKNNAVPTIFDFTCHKSM
 hTHAP0 1 MNEF-SANPACTYS---TOSDSEHPEEP-PPANCKMENC-RAD---YRTVIRONAVPTIFDFTS
 hTHAP7 1 MPRR-SNACCTDTR-TNPESTHIFPILGNPGRHIANCO-RDPS-GOGHLD
 hTHAP9 1 MTRR-SNVCSTDTVL-SHREHSHICEH-TDITQSKIRAN-RVDP-SKKIMI
 hTHAP6 1 VAC-SANICASECLPN-SLKGEMHPTENIER-KALLAK-RLDVN-AAGTME
 hTHAP11 1 MGFTCCVPCSMNHS---RDLNLEHETP-KDAELRLMFKWS-SAGVSGCFSTGO
 hTHAP10 1 MPR-SVAPACENTK---SGSLRFP-KRAVLIADRTVACGAD-AY
 dmTransposase 1 -MKY-SKFC-SKAVIG---KKLHPE-KCALIKTMEOSLG---CS---L
 consensus 1 mpk C a C nr k k vshkfp hd ir Wv v i w

hTHAP1 47 P-----TKYSSIGSEHFPTDCKRECN-----NRIKKNNAVPTIFICTEPHDK
 hTHAP3 48 P-----KQHTVIGSEHFPECE-SAPGN---RKNKKNNAVPTIFAFQDFTQ
 hTHAP5 50 P-----SKYDFLCSHFPTDSDIRWG-----VRLKPECAVPSIFSGPPAK
 hTHAP8 51 P-----SCHOLCSHFPTSCQWRWG-----VRLKPECAVPSIFSGPPAK
 hTHAP4 49 P-----TKYSEFCSHFPTDSEKLEED---CHRLKPECAVPSIFH--LTK-
 hTHAP2 46 P-----GKHTFICSHEPEASCDITGO---TR-RKNNAVPTIFDFTCHKSM
 hTHAP0 45 DKTPDLNKHVRLCASHFETSMICRTP-----YRTVIRONAVPTIFDFTS
 hTHAP7 56 P-----SEYIFCSHPEEDCEBELGIS---GYHMECAVPTIFESFS
 hTHAP9 55 PG-----FGAI-LCSHFPTDSEYIGIR-----EKKKCAVESVLYK
 hTHAP6 55 PK-----KGDV-LCSHFPTDSEYIGIR-----EKKKCAVESVLYK
 hTHAP11 54 P-----TTGHRACSHVFGG-----KATTVANPTIFPGRVNERKV
 hTHAP10 46 GG-----NDRSVICSDHFAPACDVSVI-----CKNLRFSDRLVAGAVTLL-
 dmTransposase 38 G-----ENSQICDTHENDSQKKAAPAKGQTEKRPINADAVEKVIHPEPEKI
 consensus 61 P-----icsHF f k k a vptif

[illegible]

[illegible]

Figure 10

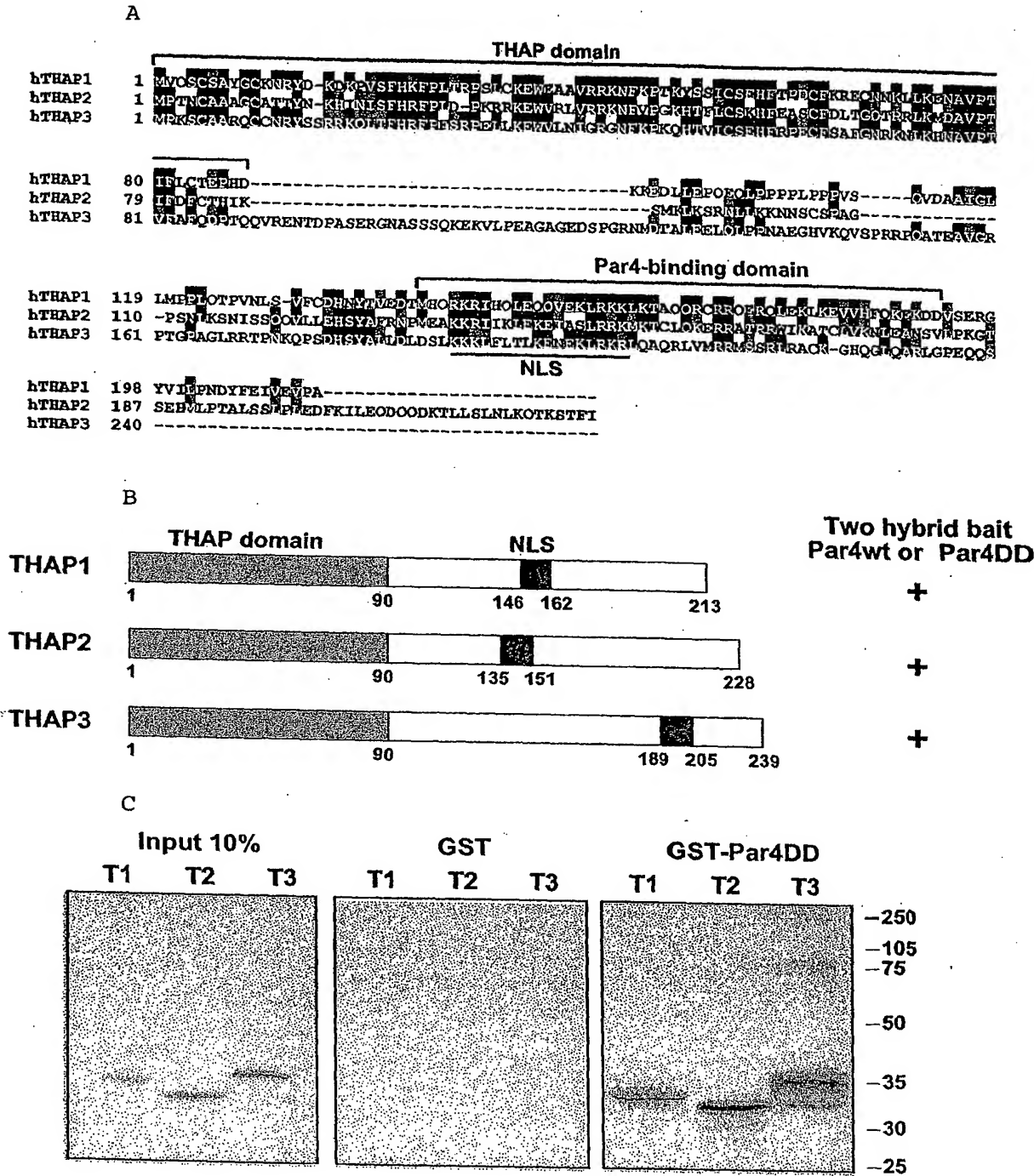


Figure 11

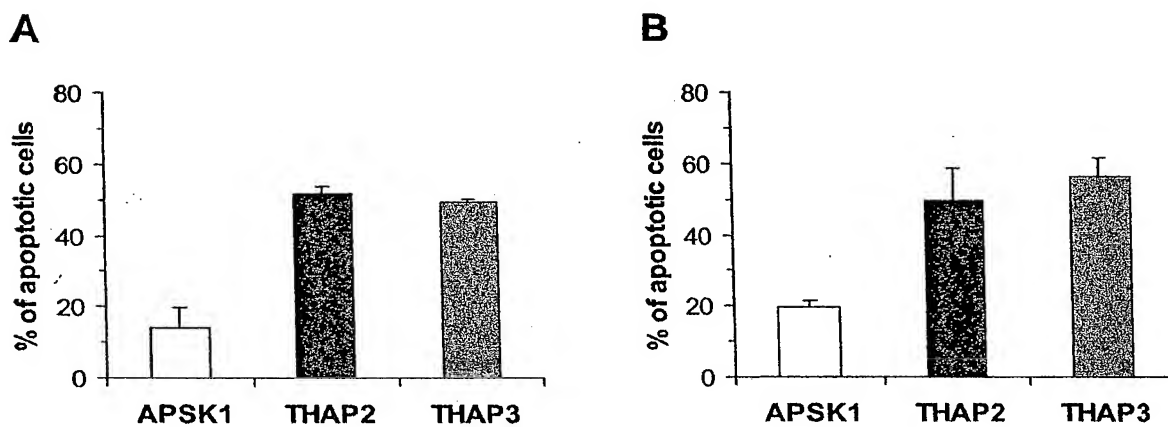


Figure 12

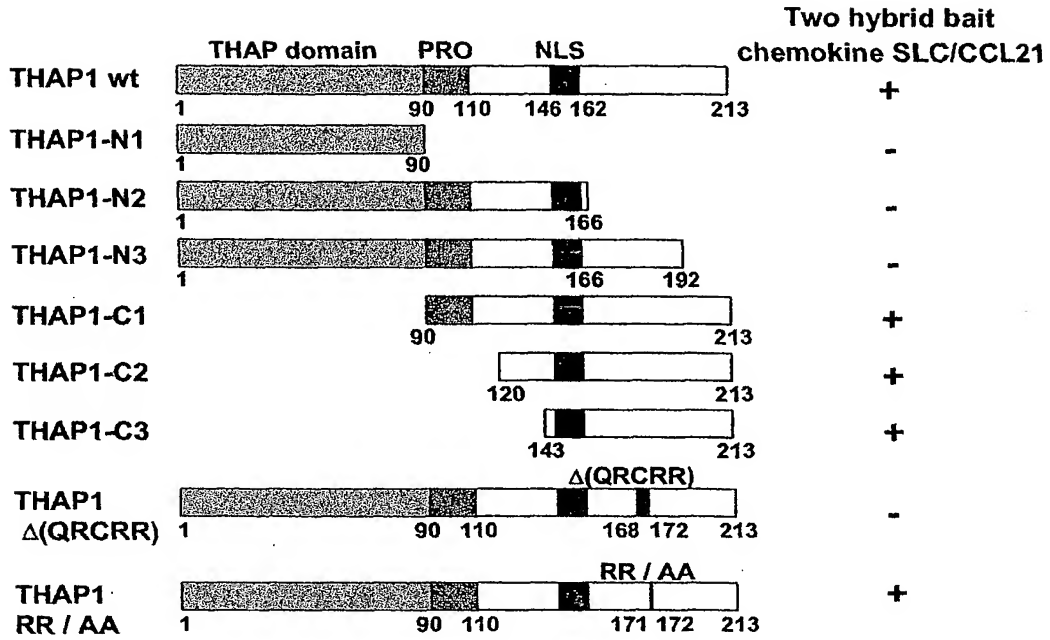
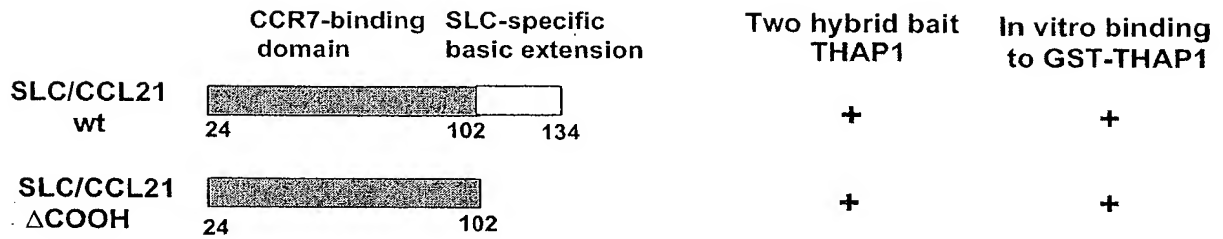
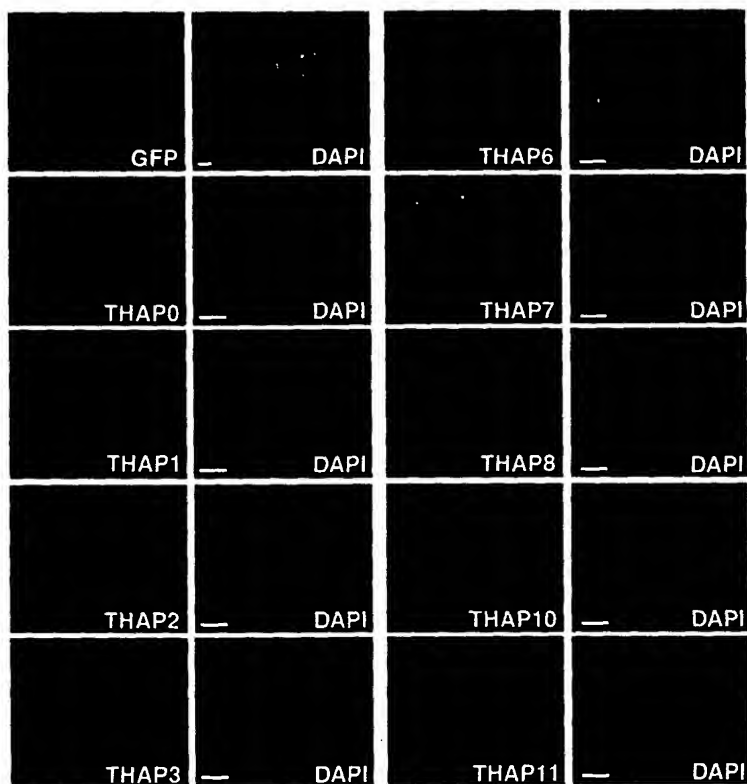


Figure 13



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FIGURE 14





A	HLLR (H360) DEL VV G GRAT HVE THAP1 (1)HVS S G KURYDEKPV HRF HLLR (H375)LHS XS KYECK VIDRVTRNO THAP1 (45)PRTRYSSI SE TRD	TRP C33 KH (H334) C33 KH (H34) AVGANTDIIV (H375) HAUPTTIF (8)	
B		THAP1	DmTRP
C			
D	GLNA (A474)HRFRT (V)SEKSS HF CV DmTRP (1) HRY R C WAT KLHV GLNA (M74)YL AGRIID LICKRRR PA VY DmTRP (42)QI DT NDSD AAPA	CSJGEHS (41) AGMLEAKRTTK (A514) ER MADADPSK (76)	

FIGURE 16

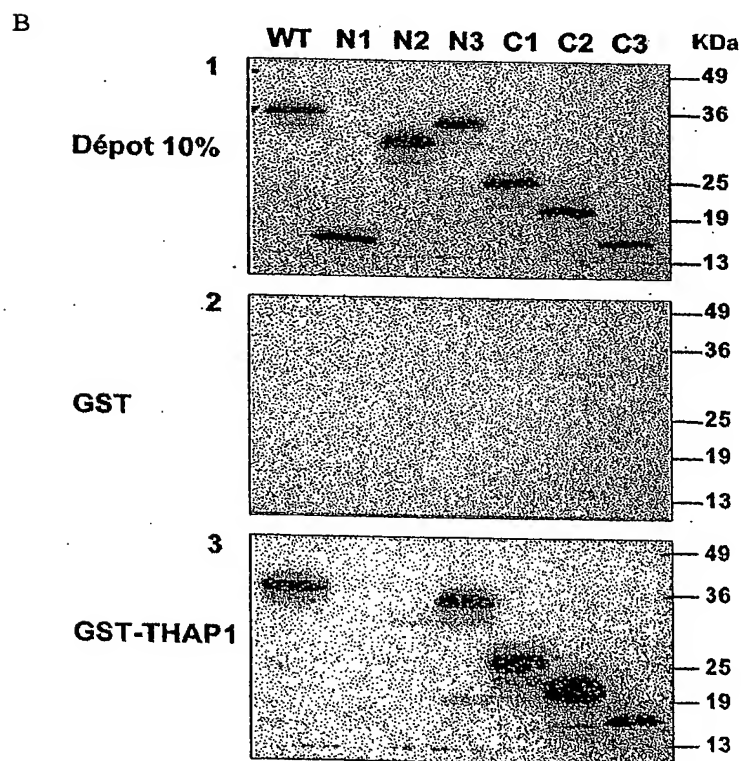
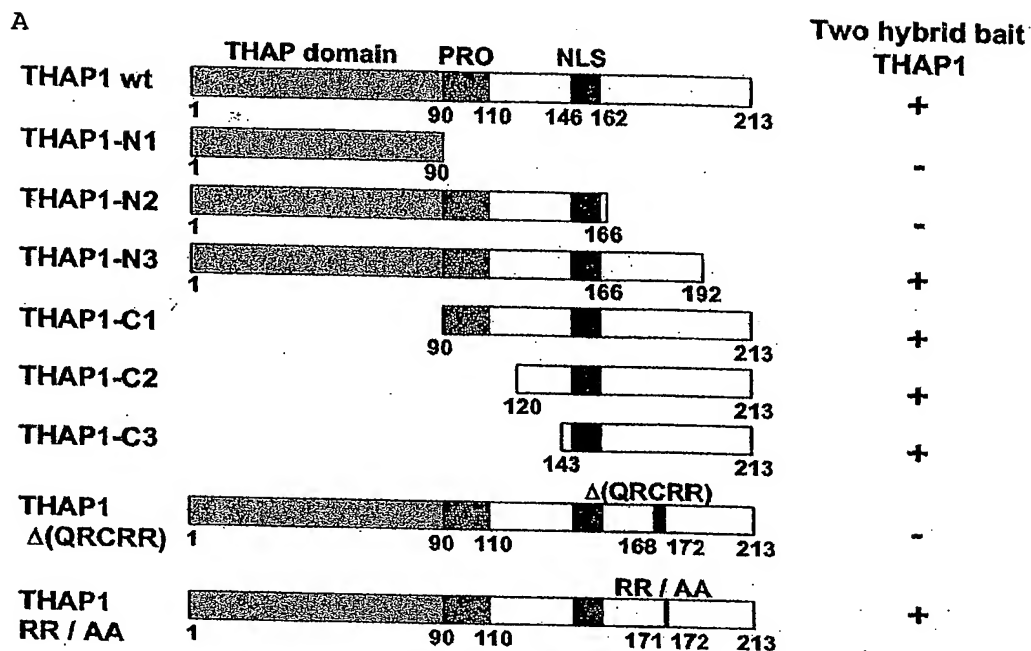


FIGURE 17

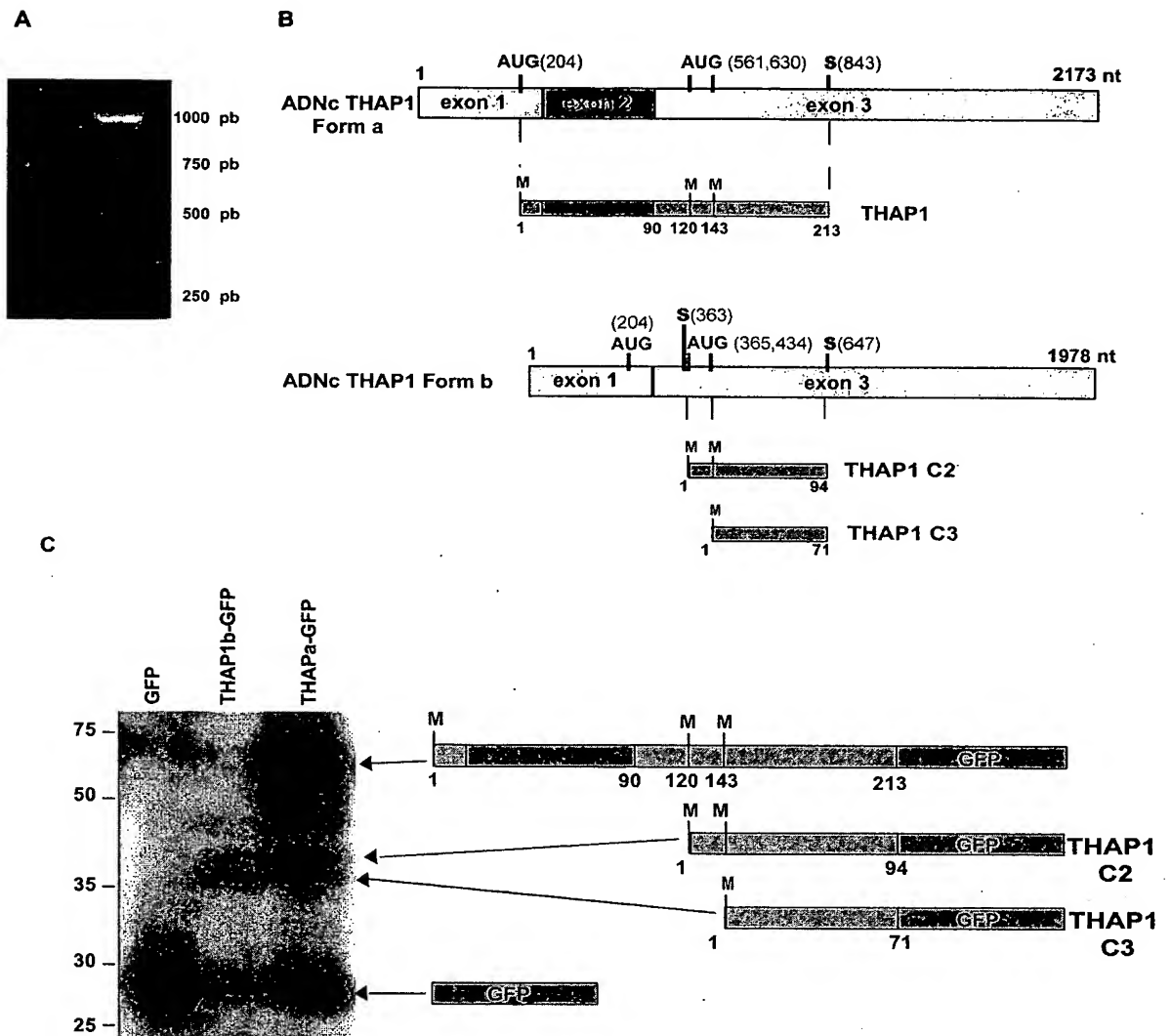


Figure 18

GGGCAT ACTAC TGGCAA
GGGCAA ACTGT GGGCAT
GGGCAT ACTAC TGGCAA
GGGCAA ACTAC TGGCAA
GGGCAA GTTCG TTGCAA
GGGCAT GTAC TGGCAA
GGGCAA CTGT GGGCAA
GGGCAA CACTAC TGGCAA
GGGCAA AGTAC TGGCAA

A

1) DR-5 Consensus Motif
GGGCAAAnnnnnnTGGCAA
(DR-4, DR-6)

TTGCCA GTACTAAGTGT GGGCAA
CTGCCA GTACATAGTGT GGGCAA
TTGCCA GTACTAAGTGT GGGCAA
CTGCCA GTAGATACTGT GGGCAA
TTGCCA GTAGTTAGGTGT GGGCGA
TTGCCA GTAGTTAGTGT GGGCAA
TTGCCA GTACCTACTAA GGGCAA
TTGCCA GTAGTTAGTGT GGGCAG
CTGCCA GTAGTAAGTGT GGGCAG

B

2) ER-11 Consensus Motif
TTGCCAnnnnnnnnnnGGGCAA
(ER-12)

Figure 19

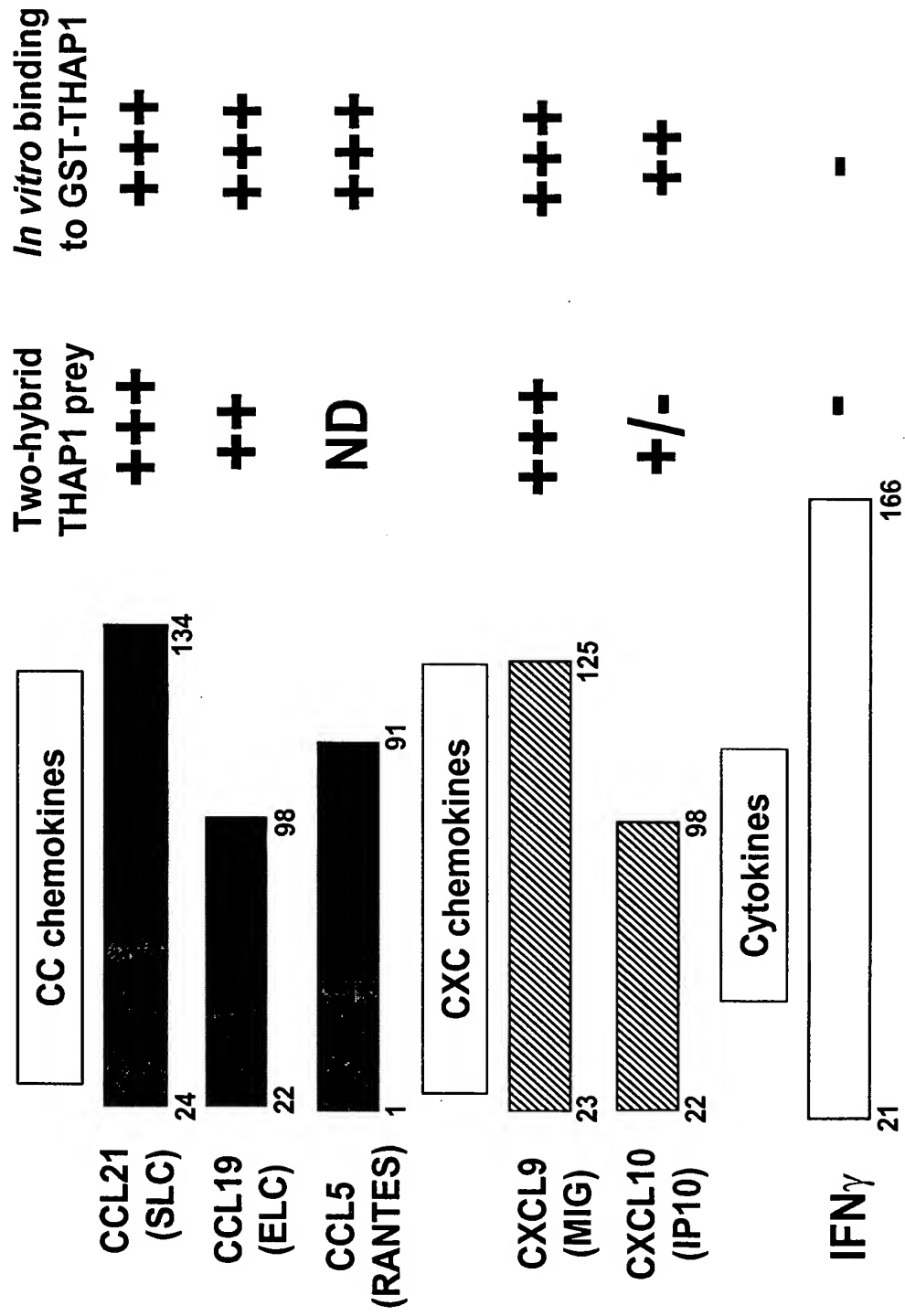


Figure 20

